

FIGURE 1

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGCTGGGA
CAAGAAGCCGCGCCTGCTGCTCCCGGCCCGGGAGGGGGCTGGGGCTGGGGCCGGAGCGG
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGCTTTGGGCACCTACCCGTGGGGGCCGTAAAGGCGCTACTATATAAGGCTGCCGGCCGGAG
CCGCGCGCGCTCAGAGCAGGAGCGCTGCTGCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCGACGCGATCCCGGTGCGCGCCAGCCTCCCGCACCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCAGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGCTCGTGGACTGCGCGCGGGGC
CAGAGCGCGCACAGTTTGTGGAGATCAAGGCAGTCCGCTCTGCGGACCGTGCCCATCAAGGG
CGTGACACGCGTGCCTACCTCTGCATGGGCGCCGACGGCAAGATGCAAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCATGCTGCCCATGGTCCCAGAGAGCCTG
AGGACCTCAGGGGCCACTTGGAAATCTGACATGTTCTCTCGCCCCCTGGAGACCGACAGCATG
GACCCATTTGGGCTTGTCACCGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAACT
GAGACCATGCCGGGCCCTTCTACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAGAGTTTTCATTGGCAGTCCAGTTTCTAGCCAAATAGACTTGTCTGAT
CATAACATTGTAAGCTGTAGCTTGCCACAGTGTGCTGGGGCCCCATTCTGCTCCCTCGA
GGTGTCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACTTCCCTTTGGAAAAATCTTATGTCAAGCTGAAATTCCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTAAATTCAGGAACAGGTGATCCACTCTGTGA
AAACAGCAGGTAAATTTCACTCAACCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTGCGCTTCCCAAATCCCTCCAGGCCAGAAGTACTGGAGCAGGCATGGCCCCACGAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGGAAATTCGCC
CTGAGGCCAGTTCTGTCATGGATGCTGTGCTGAGAATAACTTGCTGTCCCGGTGTACCTGC
TTCCATCTCCAGCCACAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCCACTTATGTCAACCTGCACTTCTTGTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCGACACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTGATATGTACA
TCTCTTATTTTCTTACATTATTTATGCCCCCAATATATTATGTATGTAGTGAGGTTTG
TTTTGTATATTAAATGGAGTTTGT

09924647-080701

FIGURE 2

MRSGCVVHVHVLWLAGLWLA VAGRPLAFSDAGPHVHYGWGDP IRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALTVAIKGVHSVRYLCMGADGKMQGLLYSEEDCAFE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVP EEPEDLRGHLES
MFSSPLETDSMDPFGLVTGLEAVRSPSEK

signal peptide:

amino acids 1-22

N-myristoylation sites:

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site:

amino acids 48-59

HBGF/FGF domain:

amino acids 80-131

0924547.080701

FIGURE 3B

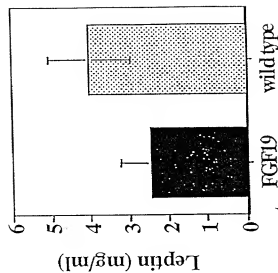


FIGURE 3A

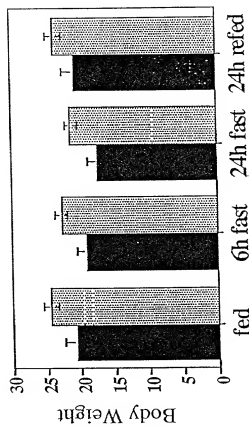


FIGURE 4A

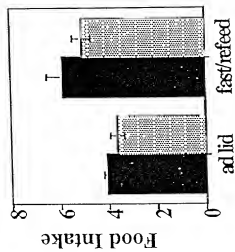


FIGURE 4B

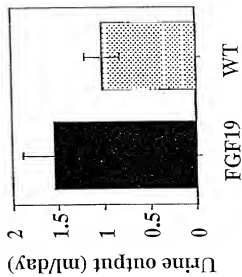
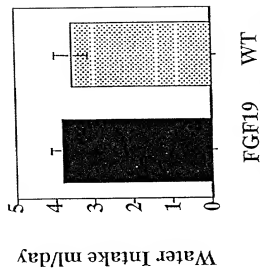


FIGURE 4C

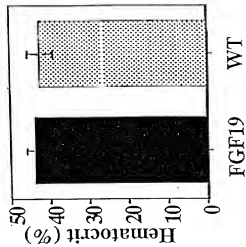


FIGURE 4D

FIGURE 5

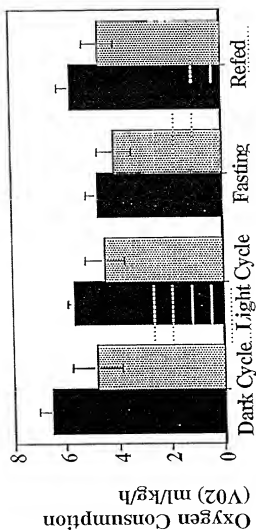


FIGURE 6B

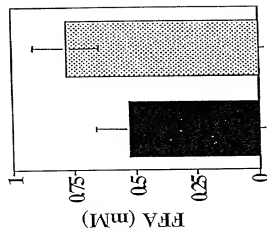


FIGURE 6A

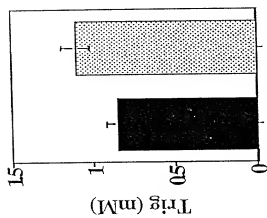


FIGURE 7A

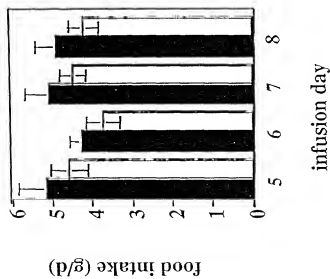


FIGURE 7B

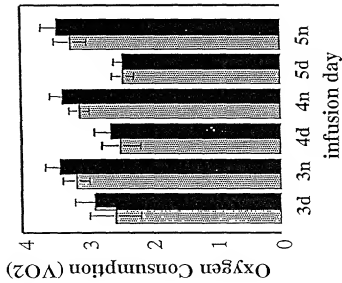


FIGURE 8A

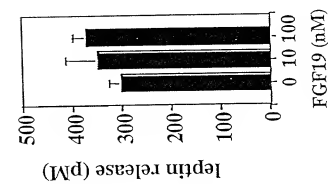
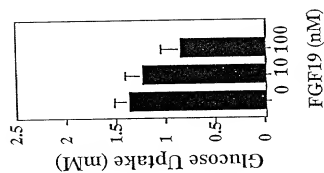


FIGURE 8B



FO2080-24942660

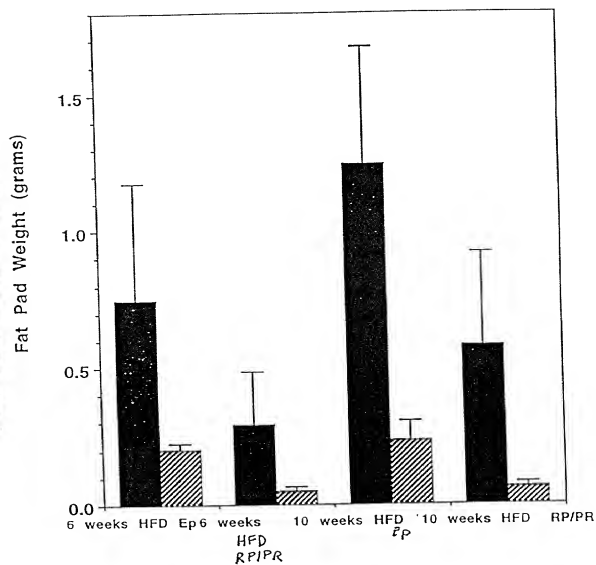


FIGURE 9

10/0801-24942660

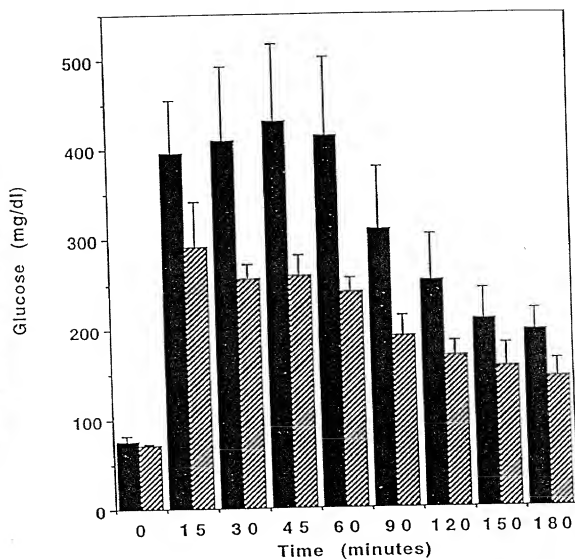


FIGURE 10

Fig. 11

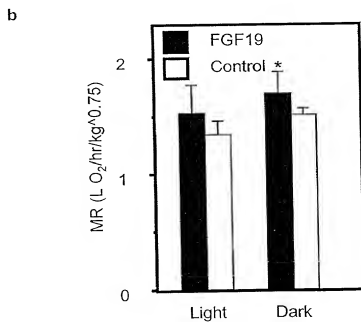
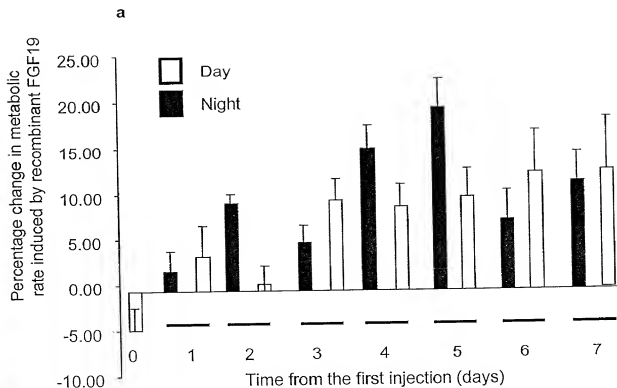


Fig 12

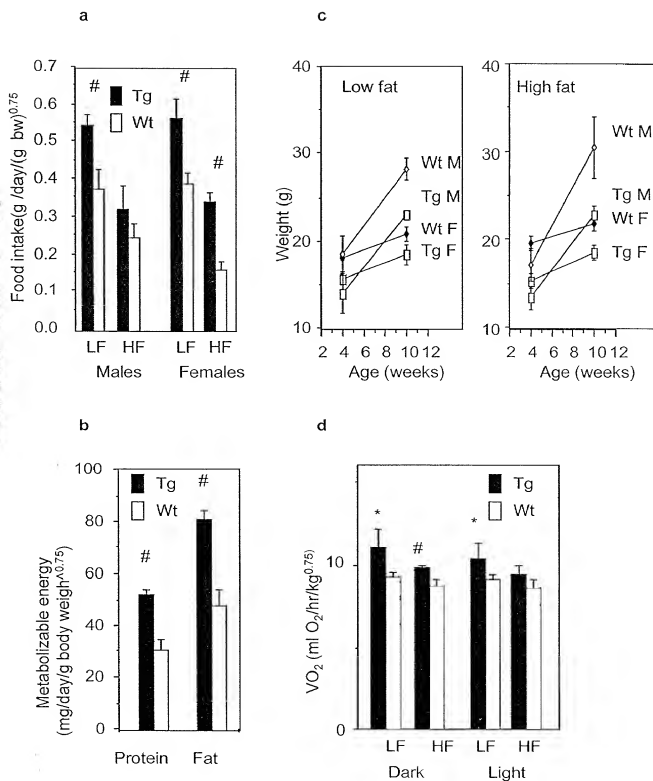


Fig. 13

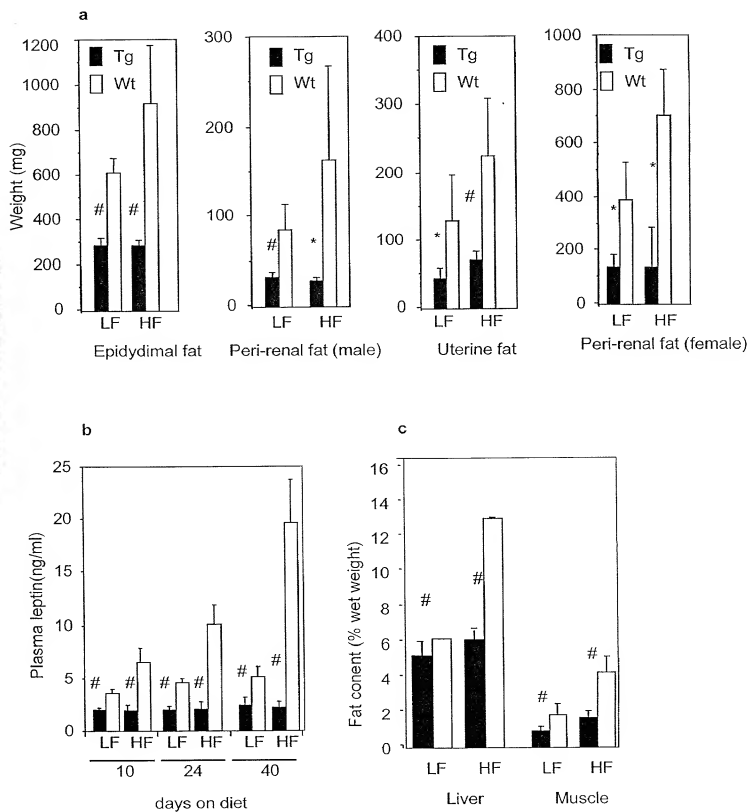


Fig. 14.

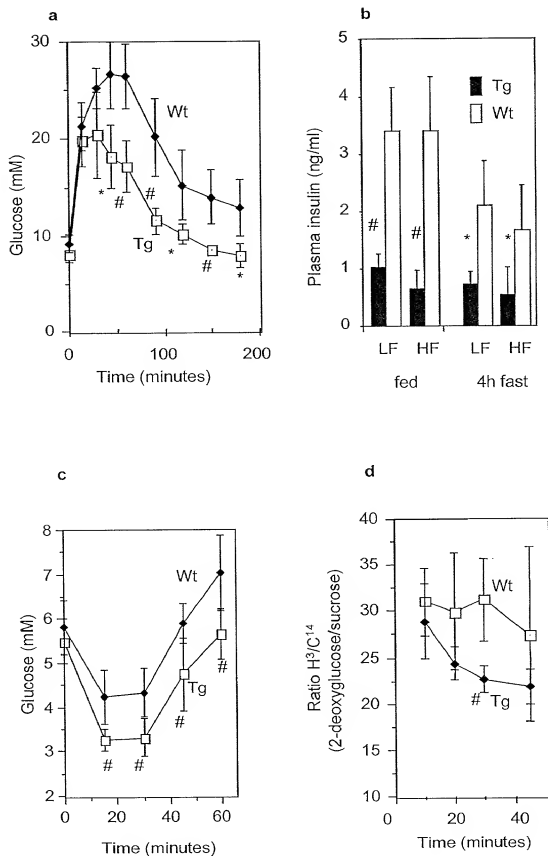


Fig. 15.

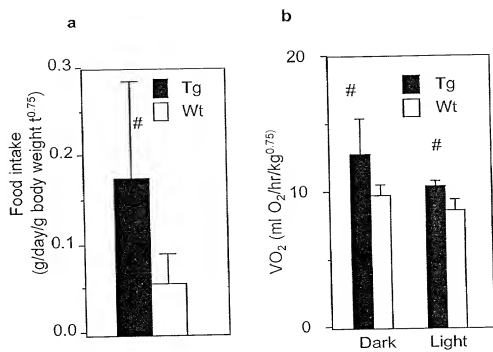
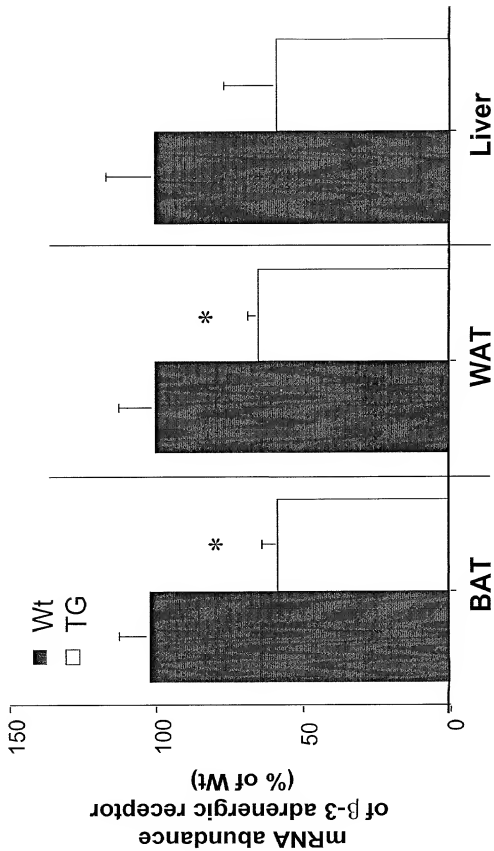
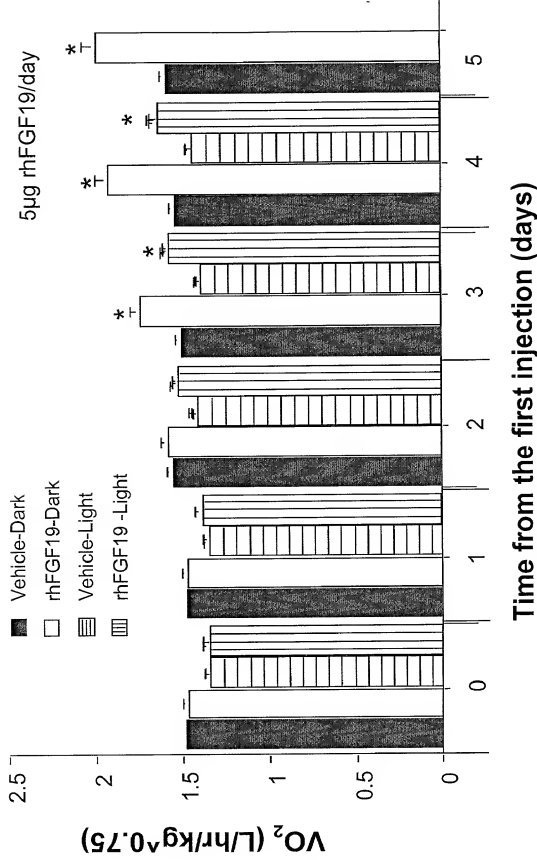


Figure 16



*P < 0.05 vs Wt controls

Figure 17



* $P < 0.05$ vs Vehicle controls with the same cycle on the same day

Figure 18

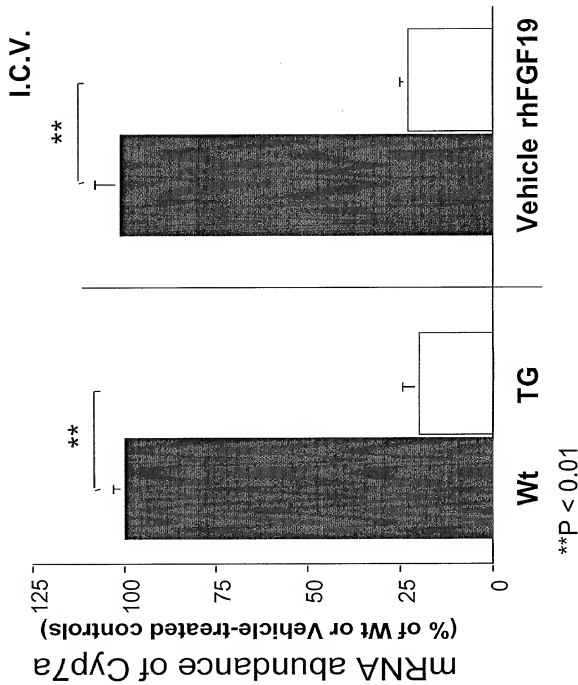


Figure 19

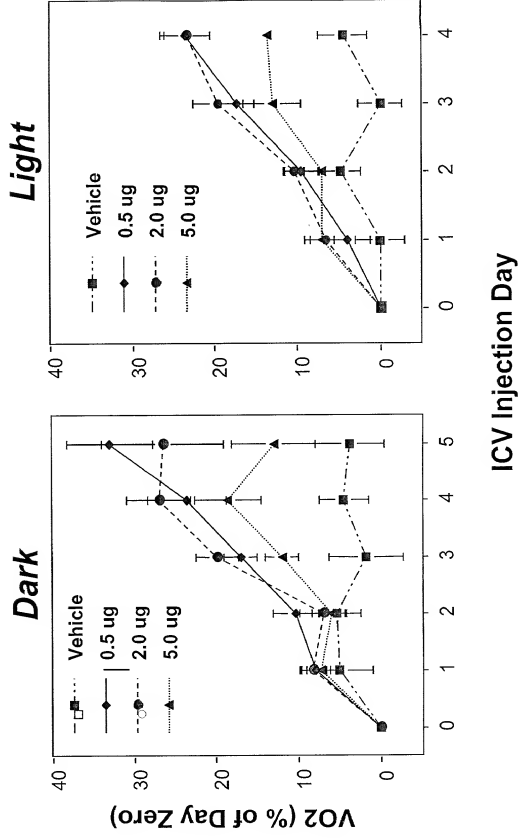


Figure 20

	<u>Vehicle</u>	<u>rhFGF19</u>		
		<u>5.0 µg</u>	<u>2.0 µg</u>	<u>0.5 µg</u>
NPY	1.0 +/- 0.08	0.81 +/- 0.23	0.63 +/- 0.20	0.40 +/- 0.08
AgRP	1.0 +/- 0.33	0.26 +/- 0.10	0.57 +/- 0.26	0.29 +/- 0.16
POMC	1.0 +/- 0.27	1.49 +/- 0.42	3.48 +/- 1.5	38.77 +/- 3.32
MC4-R	1.0 +/- 0.16	0.47 +/- 0.09	0.70 +/- 0.10	0.48 +/- 0.08

